

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel Use of EDG Receptor

<130> 3127W00P

<150> JP 2002-361415

<151> 2002-12-12

<160> 45

<210> 1

<211> 364

<212> PRT

<213> human

<400> 1

Met Ala Ala Ile Ser Thr Ser Ile Pro Val Ile Ser Gln Pro Gln Phe

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Thr Ala Met Asn Glu Pro Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe

20 25 30

Phe Tyr Asn Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val

35 40 45

Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met

50 55 60

Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe

65 70 75 80

His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe

85 90 95

Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn

100 105 110

Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile

115 120 125

Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile

130 135 140

Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
 145 150 155 160
 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
 165 170 175
 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
 180 185 190
 Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
 195 200 205
 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
 210 215 220
 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
 225 230 235 240
 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
 245 250 255
 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr
 260 265 270
 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
 275 280 285
 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
 290 295 300
 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
 305 310 315 320
 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly
 325 330 335
 Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
 340 345 350
 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val
 355 360

<210> 2

<211> 1092

<212> DNA

<213> human

<400> 2

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cttgccacag aatggaacac agtcagcaag ctggtgatgg gacttggaat cactgtttgt 180
atcttcatca tgttgcccaa cctattggtc atggtggcaa tctatgtcaa ccgccgcttc 240
cattttccta tttattacct aatggcta at ctggtgctg cagacttctt tgctgggttg 300
gcctacttct atctcatgtt caacacagga cccaatactc ggagactgac tgtagcaca 360
tggtcctgc gtcagggcct cattgacacc agcctgacgg catctgtggc caacttactg 420
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aaccggcggg tagtggtggt cattgtggtc atctggacta tggccatcgt tatgggtgct 540
ataccagtg tgggctggaa ctgtatctgt gatattgaaa attgttcaa catggcaccc 600
ctctacagtg actcttactt agtcttctgg gccattttca acttggtgac ctttgtggt 660
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cgcatagtt ctggaccccg gcggaatcgg gataccatga tgagtcttct gaagactgtg 780
gtcattgtgc ttggggcctt tatcatctgc tggactcctg gattggtttt gttacttcta 840
gacgtgtgct gtccacagtg cgacgtgctg gcctatgaga aattcttctt tctccttgct 900
gaattcaact ctgccatgaa ccccatcatt tactcctacc gcgacaaaga aatgagcgcc 960
acctttaggc agatcctctg ctgccagcgc agtgagaacc ccaccggccc cacagaaggc 1020
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cactctgtgg tt 1092

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<210> 3

<211> 364

<212> PRT

<213> Rat

<400> 3

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Met Ala Ala Ala Ser Thr Ser Ser Pro Val Ile Ser Gln Pro Gln Phe
      5              10              15
Thr Ala Met Asn Glu Gln Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
      20              25              30
Phe Tyr Asn Arg Ser Gly Lys Tyr Leu Ala Thr Glu Trp Asn Thr Val
      35              40              45
Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Val Phe Ile Met
      50              55              60
Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
      65              70              75              80
His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
      85              90              95
Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn

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100	105	110	
Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile			
115	120	125	
Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile			
130	135	140	
Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser			
145	150	155	160
Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile			
165	170	175	
Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile			
180	185	190	
Asp His Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val			
195	200	205	
Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu			
210	215	220	
Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser			
225	230	235	240
Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu			
245	250	255	
Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Val Cys Trp Thr			
260	265	270	
Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp			
275	280	285	
Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser			
290	295	300	
Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala			
305	310	315	320
Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Asn Glu Asn Pro Asn Gly			
325	330	335	
Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile			
340	345	350	
Leu Ala Gly Val His Ser Asn Asp His Ser Val Val			
355	360		

<210> 4

<211> 1092

<212> DNA

<213> Rat

<400> 4

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ctagccacag aatggaacac tgtgagcaag ctggtgatgg gactgggcat cactgtctgc   180
gtgttcacaa tgctggccaa tctactggtc atggtggcaa ttacgtcaa ccgccgcttc   240
catttccta tttattactt gatggccaac ctggctgctg cagacttctt cgctggactg   300
gcctacttct acctgatgtt caacacggga cctaataccc ggagactgac cgtgagcaca   360
tggtcttctc ggcagggcct catcgacacc agcctgacgg cttctgtggc caacctgctg   420
gccattgcca tcgagaggca catcacagtt ttccgaatgc agtccatac acgaatgagc   480
aaccgacgtg tgggtggtgt gattgtagtc atctggacta tggccattgt gatgggtgcc   540
ataccacgtg tgggctggaa ctgcatctgt gatatcgatc attgttcaa catggcgccc   600
ctctacagtg actcctactt agtcttctgg gccattttca acctgggtgac ctttgtggtc   660
atggtggttc tctacgtca catctttggc tatgttcgcc agaggactat gagaatgtcc   720
cggcatagtt ctggaccag gaggaatcgg gacaccatga tgagccttct gaagactgtg   780
gtcattgtgc tgggtgcctt tattgtctgc tggactccgg gattggtctt gctactgctc   840
gatgtgtgtt gccgcagtg cgaatgcctg gcctatgaga agttcttctt cctcctggcc   900
gagttcaact ctgctatgaa ccccatcatt tactcctacc gcgacaaaga gatgagcgcc   960
accttcaggc agatcctgtg ttgccagcgc aacgagaacc ccaacggccc cacggaaggc  1020
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<210> 5

<211> 378

<212> PRT

<213> human

<400> 5

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Met Ala Thr Ala Leu Pro Pro Arg Leu Gln Pro Val Arg Gly Asn Glu
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Thr Leu Arg Glu His Tyr Gln Tyr Val Gly Lys Leu Ala Gly Arg Leu
      20              25              30
Lys Glu Ala Ser Glu Gly Ser Thr Leu Thr Thr Val Leu Phe Leu Val
      35              40              45
Ile Cys Ser Phe Ile Val Leu Glu Asn Leu Met Val Leu Ile Ala Ile
      50              55              60

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Trp	Lys	Asn	Asn	Lys	Phe	His	Asn	Arg	Met	Tyr	Phe	Phe	Ile	Gly	Asn
65					70				75					80	
Leu	Ala	Leu	Cys	Asp	Leu	Leu	Ala	Gly	Ile	Ala	Tyr	Lys	Val	Asn	Ile
			85					90					95		
Leu	Met	Ser	Gly	Lys	Lys	Thr	Phe	Ser	Leu	Ser	Pro	Thr	Val	Trp	Phe
	100						105				110				
Leu	Arg	Glu	Gly	Ser	Met	Phe	Val	Ala	Leu	Gly	Ala	Ser	Thr	Cys	Ser
	115					120					125				
Leu	Leu	Ala	Ile	Ala	Ile	Glu	Arg	His	Leu	Thr	Met	Ile	Lys	Met	Arg
	130					135				140					
Pro	Tyr	Asp	Ala	Asn	Lys	Arg	His	Arg	Val	Phe	Leu	Leu	Ile	Gly	Met
145					150					155				160	
Cys	Trp	Leu	Ile	Ala	Phe	Thr	Leu	Gly	Ala	Leu	Pro	Ile	Leu	Gly	Trp
			165					170					175		
Asn	Cys	Leu	His	Asn	Leu	Pro	Asp	Cys	Ser	Thr	Ile	Leu	Pro	Leu	Tyr
		180						185				190			
Ser	Lys	Lys	Tyr	Ile	Ala	Phe	Cys	Ile	Ser	Ile	Phe	Thr	Ala	Ile	Leu
	195					200					205				
Val	Thr	Ile	Val	Ile	Leu	Tyr	Ala	Arg	Ile	Tyr	Phe	Leu	Val	Lys	Ser
	210					215					220				
Ser	Ser	Arg	Lys	Val	Ala	Asn	His	Asn	Asn	Ser	Glu	Arg	Ser	Met	Ala
225					230					235				240	
Leu	Leu	Arg	Thr	Val	Val	Ile	Val	Val	Ser	Val	Phe	Ile	Ala	Cys	Trp
			245						250				255		
Ser	Pro	Leu	Phe	Ile	Leu	Phe	Leu	Ile	Asp	Val	Ala	Cys	Arg	Val	Gln
		260						265				270			
Ala	Cys	Pro	Ile	Leu	Phe	Lys	Ala	Gln	Trp	Phe	Ile	Val	Leu	Ala	Val
	275						280					285			
Leu	Asn	Ser	Ala	Met	Asn	Pro	Val	Ile	Tyr	Thr	Leu	Ala	Ser	Lys	Glu
	290					295					300				
Met	Arg	Arg	Ala	Phe	Phe	Arg	Leu	Val	Cys	Asn	Cys	Leu	Val	Arg	Gly
305					310					315				320	
Arg	Gly	Ala	Arg	Ala	Ser	Pro	Ile	Gln	Pro	Ala	Leu	Asp	Pro	Ser	Arg
			325						330				335		
Ser	Lys	Ser	Ser	Ser	Ser	Asn	Asn	Ser	Ser	His	Ser	Pro	Lys	Val	Lys
		340						345				350			
Glu	Asp	Leu	Pro	His	Thr	Asp	Pro	Ser	Ser	Cys	Ile	Met	Asp	Lys	Asn

355 360 365
 Ala Ala Leu Gln Asn Gly Ile Phe Cys Asn
 370 375

<210> 6
 <211> 1134
 <212> DNA
 <213> human

<400> 6
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 ctcaccaccg tgctcttctt ggtcatctgc agcttcatcg tcttgagaa cctgatggtt 180
 ttgattgcc a tctggaaaa caataaat t cacaaccgca tgtacttttt cattggcaac 240
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 aagaagacgt tcagcctgtc tcccacggtc tggttcctca gggagggcag tatgttcgtg 360
 gcccttgggg cgtccacctg cagcttactg gccatcgcca tcgagcggca cttgacaatg 420
 atcaaaatga ggccttacga cgccaacaag aggcaccgcg tcttctctct gatcgggatg 480
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 atcagcatct tcacggccat cctggtgacc atcgtgatcc tctacgcacg catctacttc 660
 ctggtgaagt ccagcagccg taagggtggc aaccacaaca actcggagcg gtccatggca 720
 ctgctgcgga ccgtggtgat tgtggtgagc gtgttcatcg cctgctggtc cccactcttc 780
 atctcttcc tcattgatgt ggcctgcagg gtgcaggcgt gccccatcct cttcaaggct 840
 cagtgttca tcgtgttggc tgtgtcaac tccgccatga acccggtcat ctacacgctg 900
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<210> 7
 <211> 222
 <212> PRT
 <213> Rat

<400> 7
 Arg Met Tyr Phe Phe Ile Gly Asn Leu Ala Leu Cys Asp Leu Leu Ala

8/23

5	10	15
Gly Ile Ala Tyr Lys Val Asn Ile Leu Met Ser Gly Arg Lys Thr Phe		
20	25	30
Ser Leu Ser Pro Thr Val Trp Phe Leu Arg Glu Gly Ser Met Phe Val		
35	40	45
Ala Leu Gly Ala Ser Thr Cys Ser Leu Leu Ala Ile Ala Ile Glu Arg		
50	55	60
His Leu Thr Met Ile Lys Met Arg Pro Tyr Asp Ala Asn Lys Lys His		
65	70	75
Arg Val Phe Leu Leu Ile Gly Met Cys Trp Leu Ile Ala Phe Ser Leu		
85	90	95
Gly Ala Leu Pro Ile Leu Gly Trp Asn Cys Leu Glu Asn Phe Pro Asp		
100	105	110
Cys Ser Thr Ile Leu Pro Leu Tyr Ser Lys Lys Tyr Ile Ala Phe Leu		
115	120	125
Ile Ser Ile Phe Thr Ala Ile Leu Val Thr Ile Val Ile Leu Tyr Ala		
130	135	140
Arg Ile Tyr Phe Leu Val Lys Ser Ser Ser Arg Arg Val Ala Asn His		
145	150	155
Asn Ser Glu Arg Ser Met Ala Leu Leu Arg Thr Val Val Ile Val Val		
165	170	175
Ser Val Phe Ile Ala Cys Trp Ser Pro Leu Phe Ile Leu Phe Leu Ile		
180	185	190
Asp Val Ala Cys Arg Ala Lys Glu Cys Ser Ile Leu Phe Lys Ser Gln		
195	200	205
Trp Phe Ile Met Leu Ala Val Leu Asn Ser Ala Met Asn Pro		
210	215	220

<210> 8

<211> 666

<212> DNA

<213> Rat

<400> 8

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aaggtcaaca ttctgatgtc cggttaggaag acgttcagcc tgtctccaac agtgtggttc	120
ctcagggagg gcagtatgtt cgtagccctg ggcgcatcca catgcagctt attggccatt	180


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gccattgagc ggcacctgac catgatcaag atgaggccgt acgacgcaa caagaagcac 240
cgcggtgttcc ttctgattgg gatgtgctgg ctaattgcct tctcgctggg tgccctgccc 300
atcctgggct ggaactgcct ggagaacttt cccgactgct ctaccatctt gcccctctac 360
tccaagaaat acattgcctt tctcatcagc atcttcacag ccattctggt gaccatcgtc 420
atcttgtacg cgcgcatcta cttcctggtc aagtccagca gccgcagggt ggccaaccac 480
aactccgaga gatccatggc ccttctgcgg accgtagtga tcgtggtgag cgtgttcac 540
gcctgttggt cccccctttt catcctcttc ctcacgatg tggcctgcag ggccaaggag 600
tgctccatcc tcttcaagag tcagtggttc atcatgctgg ctgtcctcaa ctccgccatg 660
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<210> 9

<211> 353

<212> PRT

<213> human

<400> 9

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Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
      20              25              30
Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
      85              90              95
Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
     100             105             110
Ser Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
     115             120             125
Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
     130             135             140
Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
     145             150             155             160
Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu

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165	170	175
Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu		
180	185	190
Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu		
195	200	205
Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala		
210	215	220
Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly		
225	230	235
Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp		
245	250	255
Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr		
260	265	270
Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr		
275	280	285
Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln		
290	295	300
Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr		
305	310	315
Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg		
325	330	335
Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val		
340	345	350
Val		

<210> 10

<211> 1059

<212> DNA

<213> human

<400> 10

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gtcatcctct gttgcgcat tgtggtggaa aaccttctgg tgctcattgc ggtggcccga	180
aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta	240
ctggcaggcg tggccttcgt agccaatacc ttgctctctg gctctgtcac gctgaggctg	300
acgcctgtgc agtggtttgc ccgggagggc tctgcctcca tcacgctctc ggcctctgtc	360

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ggcagcgaca agagctgccg catgtttctg ctcatcgggg cctcgtggct catctcgctg 480
gtcctcggtg gcctgcccac ccttggcttg aactgccttg gccacctcga ggcctgctcc 540
actgtcctgc ctctctacgc caagcattat gtgctgtgcg tggtgacctt cttctccatc 600
atcctgttgg ccatcgtggc cctgtacgtg cgcacttact gcgtgggtccg ctcaagccac 660
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cggccgctgc agtgcctggc gccgggggtg ggggtgcaag gacggaggcg ggtcgggacc 960
ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1020
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<210> 11

<211> 352

<212> PRT

<213> Rat

<400> 11

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Met Gly Gly Leu Tyr Ser Glu Tyr Leu Asn Pro Glu Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Asp Met Gln Glu Thr Pro Ser
      20              25              30
Arg Lys Val Ala Ser Ala Phe Ile Ile Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Pro Val
      85              90              95
Thr Leu Ser Leu Thr Pro Leu Gln Trp Phe Ala Arg Glu Gly Ser Ala
      100             105             110
Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
      115             120             125
Glu Arg Gln Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
      130             135             140

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Ser Cys Arg Met Leu Met Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
 145 150 155 160
 Ile Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Asp His Leu
 165 170 175
 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
 180 185 190
 Cys Val Val Thr Ile Phe Ser Val Ile Leu Leu Ala Ile Val Ala Leu
 195 200 205
 Tyr Val Arg Ile Tyr Phe Val Val Arg Ser Ser His Ala Asp Val Ala
 210 215 220
 Gly Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
 225 230 235 240
 Val Phe Ile Ile Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
 245 250 255
 Ser Thr Cys Pro Val Arg Ala Cys Pro Val Leu Tyr Lys Ala His Tyr
 260 265 270
 Phe Phe Ala Phe Ala Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
 275 280 285
 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Leu
 290 295 300
 Cys Trp Arg Gln Gly Lys Gly Ala Thr Gly Arg Arg Gly Gly Asn Pro
 305 310 315 320
 Gly His Arg Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg Gly
 325 330 335
 Leu His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val Val
 340 345 350

<210> 12

<211> 1056

<212> DNA

<213> Rat

<400> 12

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 atcattttat gctgtgccat cgtgggtggag aaccttctgg tgctaatacgc agtggccagg 180
 aacagcaagt tccactcagc catgtacctg ttccctcgga acctggcagc ctccgacctg 240

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actcccttgc agtggtttgc ccgagagggt tcagccttca tcacgtcttc tgcctcggtc 360
ttcagcctcc tggccattgc catcgagaga caagtggcca tcgccaaggt caagctctac 420
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27